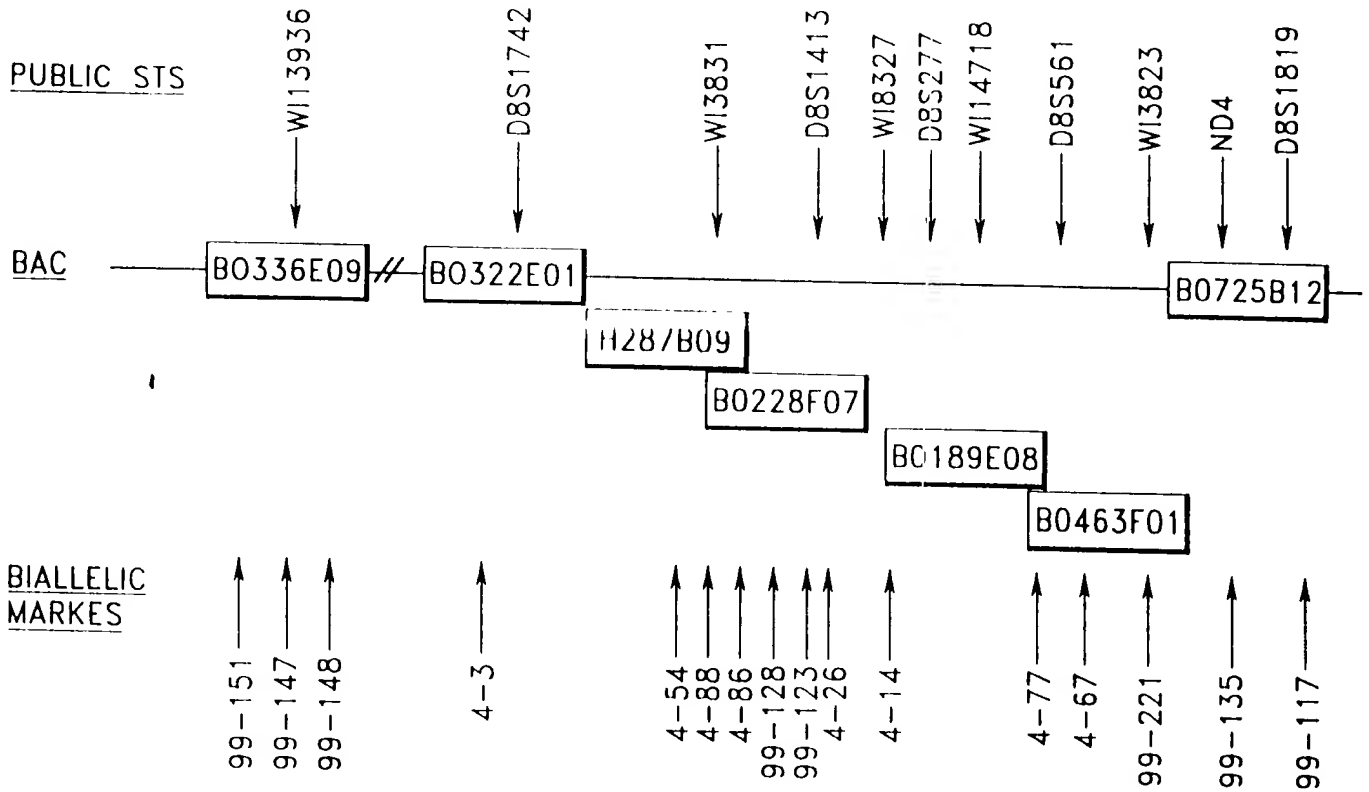

PUBLIC STS
WI13936
D8S1742
WI3831
D8S1413
WI8327
D8S277
WI14718
D8S561
WI3823
ND4
D8S1819
BAC
B0336E09
B0322E01
B0725B12
H28/B09
B0228F07
B0189E08
B0463F01
BIALLELIC MARKES
99-151
99-147
99-148
4-3
4-54
4-88
4-86
99-128
99-123
4-26
4-14
4-77
4-67
99-221
99-135
99-117

FIG. 1

ASSOCIATION STUDIES (FIRST SCREENING)

POPULATION SAMPLE SIZE	AFFECTED CASES= 112	NON AFFECTED CONTROLS=76
POPULATION CHARACTERISTICS	35 SPORADIC CASES +77 FAMILIAL CASES	>65 YEARS PSA<4

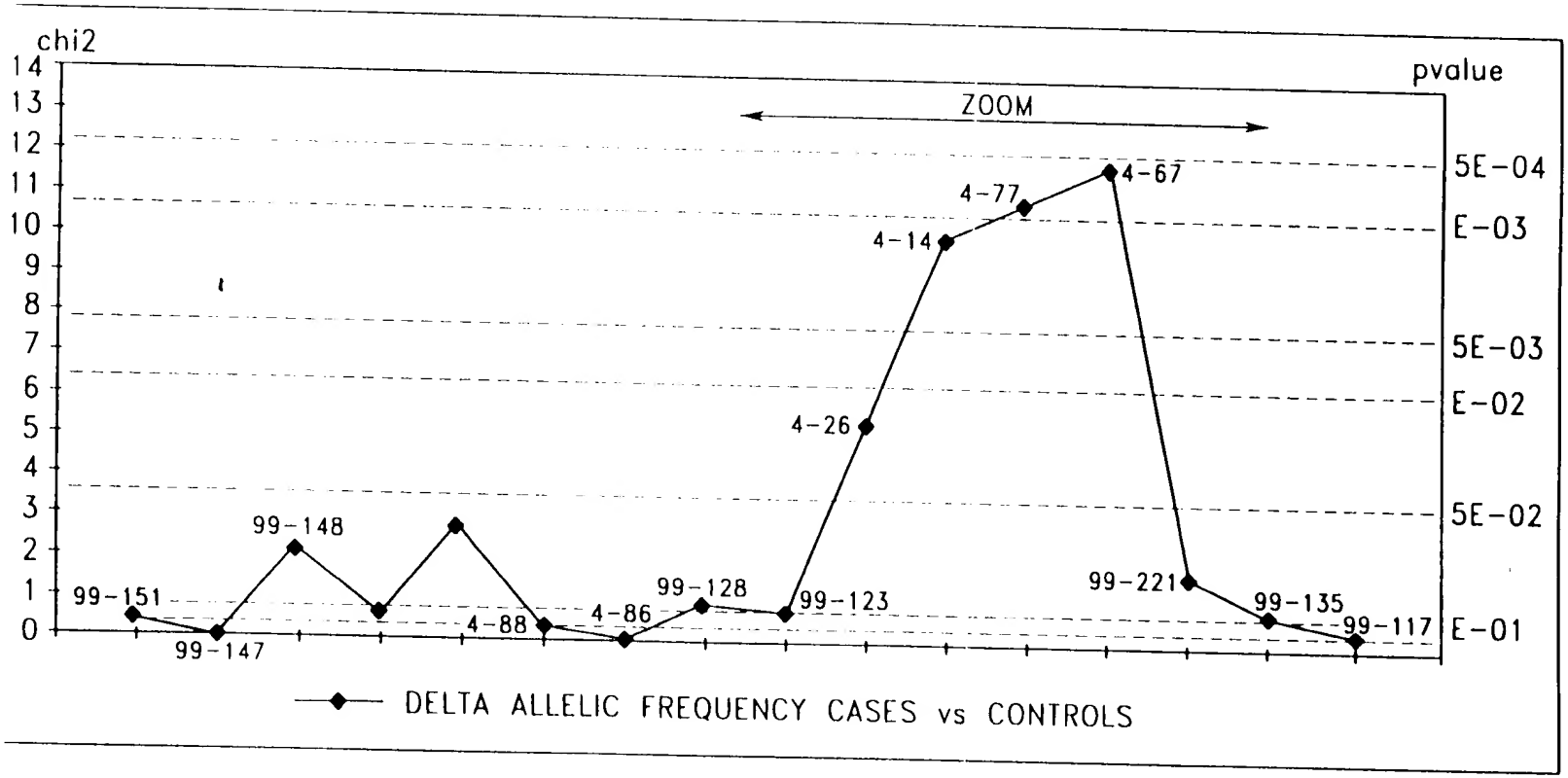


FIG.2

ASSOCIATION STUDIES (ZOOM)

	AFFECTED	UNAFFECTED
	CASES (185)	CONTROLS (104)
CHARACTERISTICS OF POPULATIONS	47 SPORADIC CASES +138 FAMILIAL CASES	>65 YEARS PSA<4

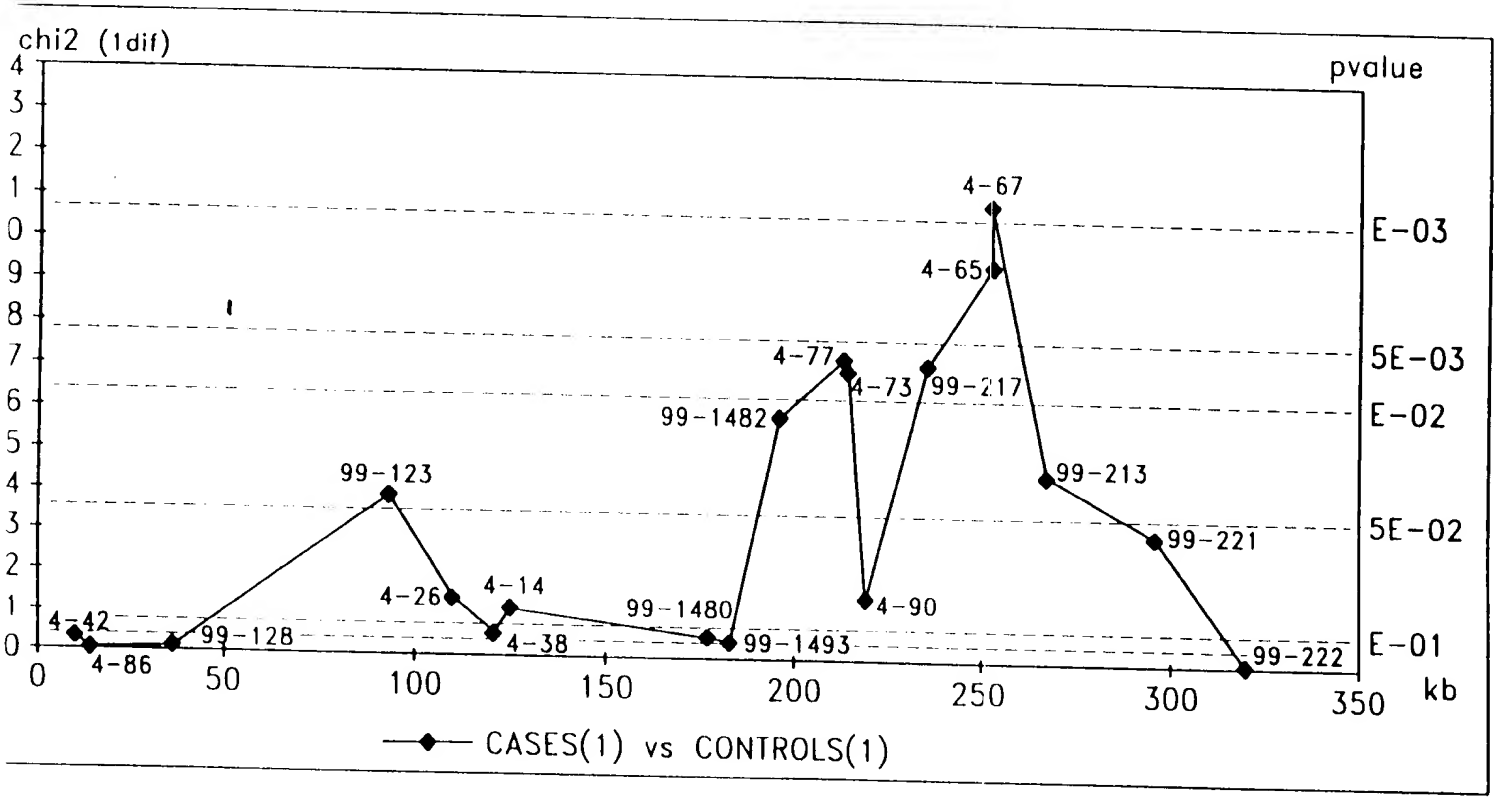


FIG.3

HAPLOTYPE FREQUENCY ANALYSIS

JLATIONS

	AFFECTED	UNAFFECTED
	CASES 2 (281)	CONTROLS 3 (130)
CHARACTERISTICS OF POPULATIONS	143 SPORADIC CASES +138 FAMILIAL CASES	>65 YEARS PSA<4

MARKERS	99-123	4-26	4-14	4-77	99-217	4-67	99-213	99-221	99-135	HAPLOTYPE FREQUENCIES		RELATIVE RISK	PVALUE
BACS	H0287B09	B0189E08		B0463F01					B0725B12				
CONTIGS	11453												
GENES	◄ PG1 ►												
VALUE	2,00E-01 *	1,00E-01 *	1,00E-01 *	2,00E-02 **	2,00E-02 **	6,00E-04 ***	9,00E-02 *	7,00E-01	2,00E-01 *	CASES (2)	CONTROLS (3)		
E BETWEEN MARKERS(KB)		<18KB>	<15KB>	<88KB>	<22KB>	<17KB>	<15KB>	<29KB>	>100KB<				
OTYPE 8>304KB<	C	A	C	G	T	T	G	A	A	0,075	0,018	4,42	9,00E-04 ***
OTYPE 7>286KB<		A	C	G	T	T	G	A	A	0,095	0,016	6,46	6,00E-05 ****
OTYPE 6<186KB>		A	C	G	T	T	G	A		0,116	0,019	6,78	1,00E-05*****
OTYPE 5<171KB>			**C**	**G**	**T**	**T**	**G**	**A**		**0,117**	**0,013**	**10,06**	**9,00E-07*******
OTYPE 4<83KB>				G	T	T	G	A		0,117	0,025	5,17	2,00E-05*****
OTYPE 3.1<54KB>					T	T	G	A		0,117	0,027	4,78	2,00E-05*****
OTYPE 3.2<54KB>				G	T	T	G			0,222	0,109	2,33	4,00E-05*****
OTYPE 2.2<39KB>				G	T	T				0,251	0,134	2,17	2,00E-04****
OTYPE 2<32KB>					T	T	G			0,226	0,112	2,32	1,00E-04***
OTYPE 1.1<17KB>					T	T				0,256	0,146	2,01	3,00E-04****
OTYPE 1.2<15KB>						T	G			0,233	0,129	2,05	6,00E-04***

FIG. 4

HAPLOTYPE SIMULATIONS (100 ITERATIONS)

MARKERS	4-144-77	99-217	4-67	99-213	99-221	HAPLOTYPE FREQUENCIES		RELATIV	PVALUE
HAPLOTYPE	C G	T	T	G	A	CASES	CONTROLS	RISK	
						0,117	0,013	10,06	9,00E-07

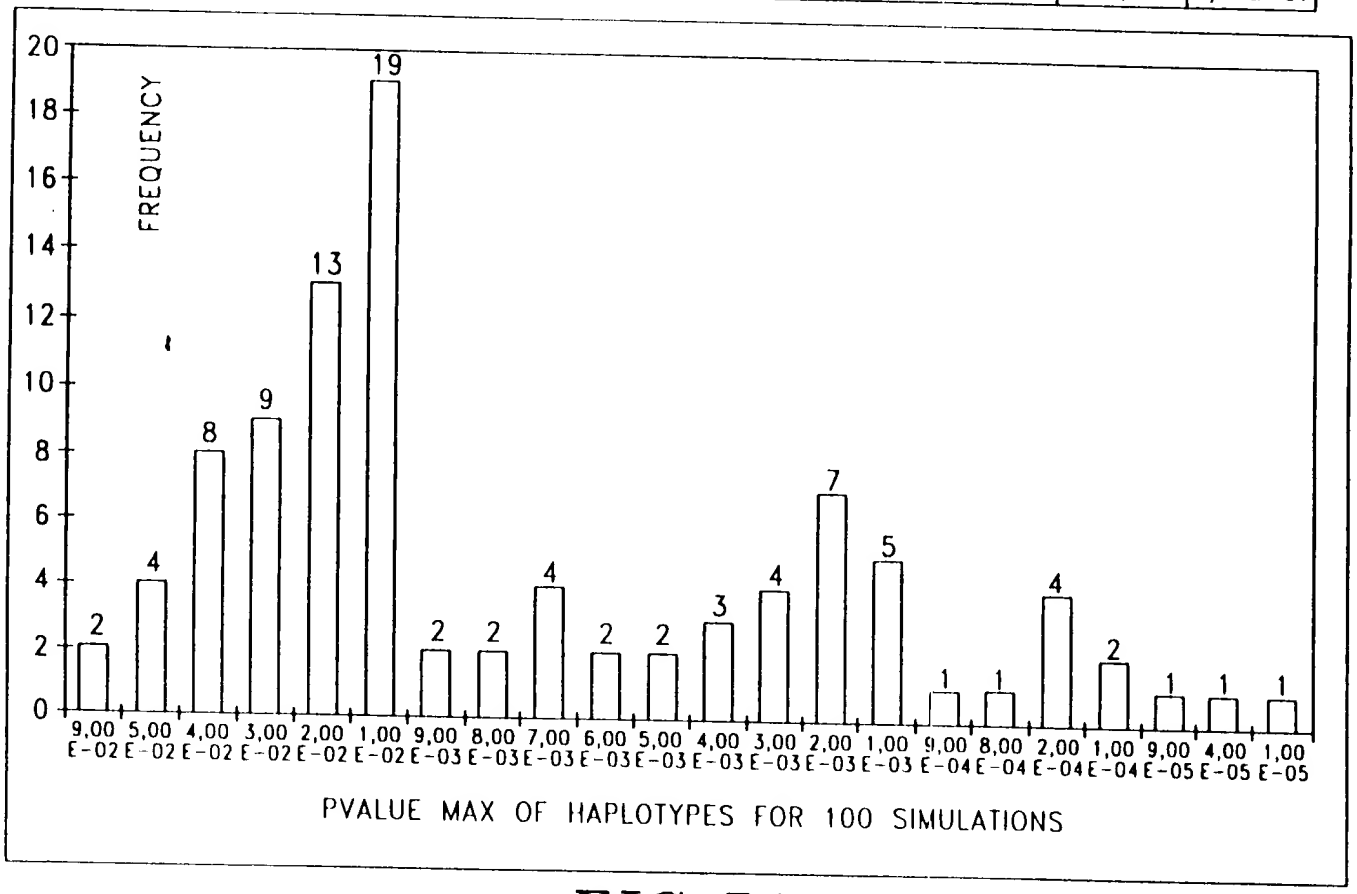


FIG.5A

HAPLOTYPE SIMULATIONS (100 ITERATIONS)

MARKERS	4-144-77	99-2174-67	99-213	99-221	HAPLOTYPE FREQUENCIES CASES	CONTROLS	RELATIV RISK	PVALUE
HAPLOTYPE	C G	T T	G	A	0,117	0,013	10,06	9,00E-07

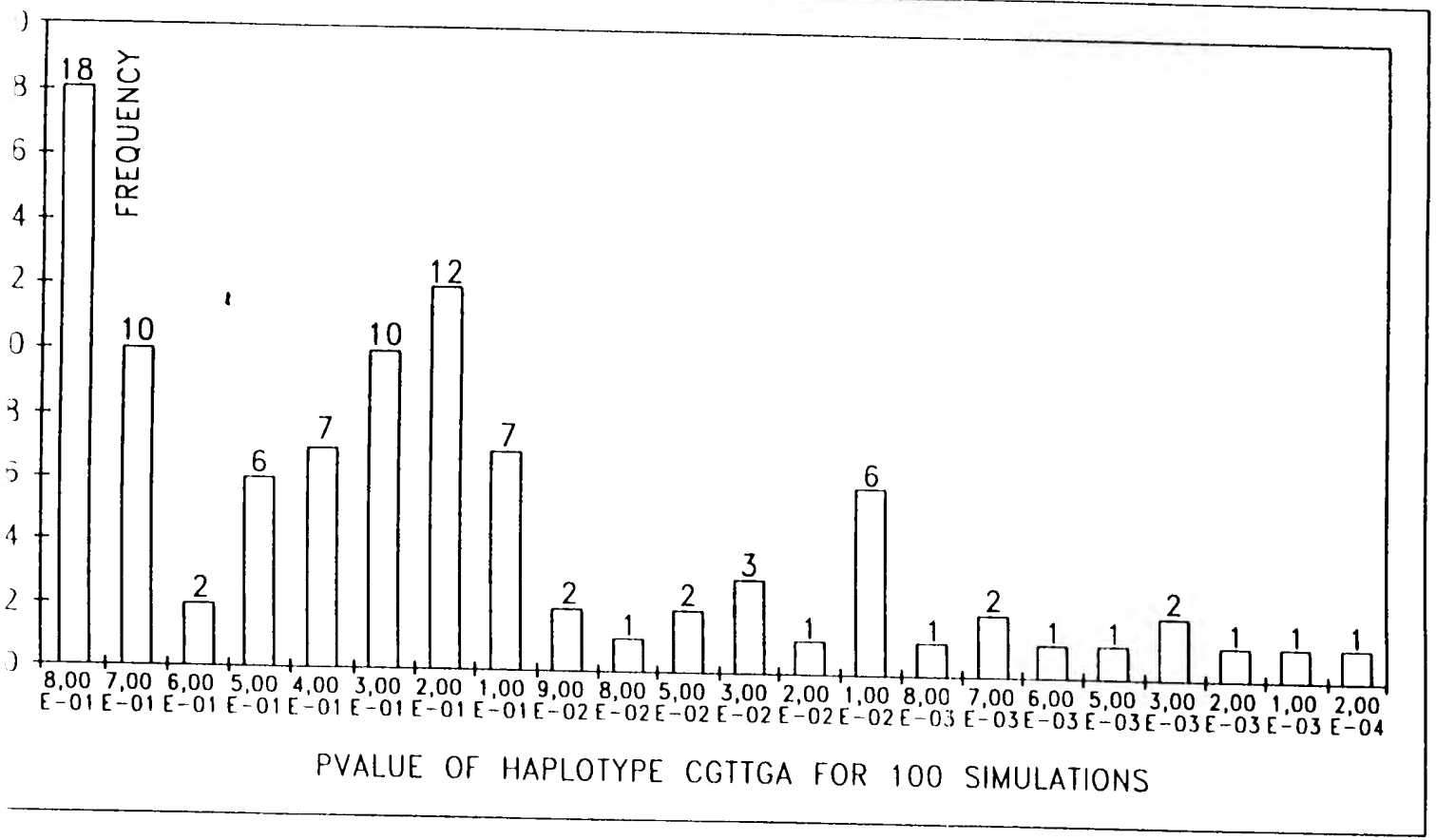


FIG.5B

C	MARKER	SEQ ID N°	SEQ ID N°(MUT)	PU SEQUENCE	SEQ ID N°	RP SEQUENCE	SEQ ID N°	POLYMORPHISM POSITION*	BASE	MICROSEQ. OLIGOS POSITIONS*	
8	99-123	21	30	AAAGCCAGGACTAGAAGG	39	TATTCAGAAAGGAGTGGG	48	24	C/T	1-23	25-47 (COMPLEMENTARY)
9	4-26	22	31	TACAGCCCTGTAAGACAC	40	TGAGGACTGCTAGGAAAG	49	24	A/G	1-23	25-47 (COMPLEMENTARY)
189	4-14	23	32	TCTAACCTCTCATCCAAC	41	GACTGTATCCTTTGATGCAC	50	24	C/T	1-23	25-47 (COMPLEMENTARY)
463	4-77	24	33	TGTTGATTTACAGGCGGC	42	GGAAAGGTACTCATTCATAG	51	24	G/C	1-23	25-47 (COMPLEMENTARY)
3	99-217	25	34	GGTGGGAATTTACTATATG	43	GTTTATTTTGTGTGAGCTTTG	52	24	C/T	1-23	25-47 (COMPLEMENTARY)
463	4-67	26	35	AAGTTCACCTTCTCAAGC	44	TGAAAGAGTTTATTCTCTGG	53	24	C/T	1-23	25-47 (COMPLEMENTARY)
3	99-213	27	36	ATACTGGCAGCGTGTGCTTC	45	TTATTGCCCCACATGCTTGAG	54	24	C/T	1-23	25-47 (COMPLEMENTARY)
3	99-221	28	37	CCCTTTTTCTTCACTGTTC	46	TCATTCGTCTGGCTAGGTC	55	24	A/C	1-23	25-47 (COMPLEMENTARY)
5	99-135	29	38	TGGAAGTTGTTATTGCCC	47	AAACACCTCCCATTGTGC	56	24	A/G	1-23	25-47 (COMPLEMENTARY)

FIG. 6A

SITIONS ARE GIVEN RELATIVE TO THE SEQUENCE OF THE CORRESPONDING MARKER (i.e. SEQ ID N°21-38 AND 57-62)

C	MARKER	SEQ ID N°	SEQ ID N°(MUT)	PU SEQUENCE	SEQ ID N°	RP SEQUENCE	SEQ ID N°	POLYMORPHISM POSITION*	BASE	MICROSEQ. OLIGOS POSITIONS*	
463	99-1482	57	60	ATCAAATCAGTGAAGTCTGAG	63	ACAAATCTATATAAGGCTGG	66	24	A/C	1-23	25-47 (COMPLEMENTARY)
3	4-73	58	61	ATCGCTGGAACATTCTGG	64	CTCTTGGTTAAACAGCAGTG	67	24	G/C	1-23	25-47 (COMPLEMENTARY)
3	4-65	59	62	GATTTAAGCTACGCTATTAG	65	TGGCTCTGCATTTCTTCC	68	24	C/T	1-23	25-47 (COMPLEMENTARY)

FIG. 6B

SITIONS ARE GIVEN RELATIVE TO THE SEQUENCE OF THE CORRESPONDING MARKER (i.e. SEQ ID N°21-38 AND 57-62)

EXON Phase	START	END	5' SPsite	PHASE	3' SPsite
Ex1 +0	2001	2216			GTGAGC
Ex2 +1	18196	18265	TAG	+0	GTTTGTA
Ex3 +0	23717	23832	CAG	+2	GTAACT
Ex4 +0	25571	25660	CAG	+0	GTAAGA
Ex5 +2	34669	34759	CAG	+0	GTAAGT
Ex6 +1	40688	40846	TAG	+1	GTAAGT
Ex7 +2	48070	48193	TAG	+2	GTGAGT
Ex8	50182	54523	TAG	+1	
ATG codon	2031	2033			
STOP codon	50405	50407			
POLY Ad site	54445	54450			

FIG. 7

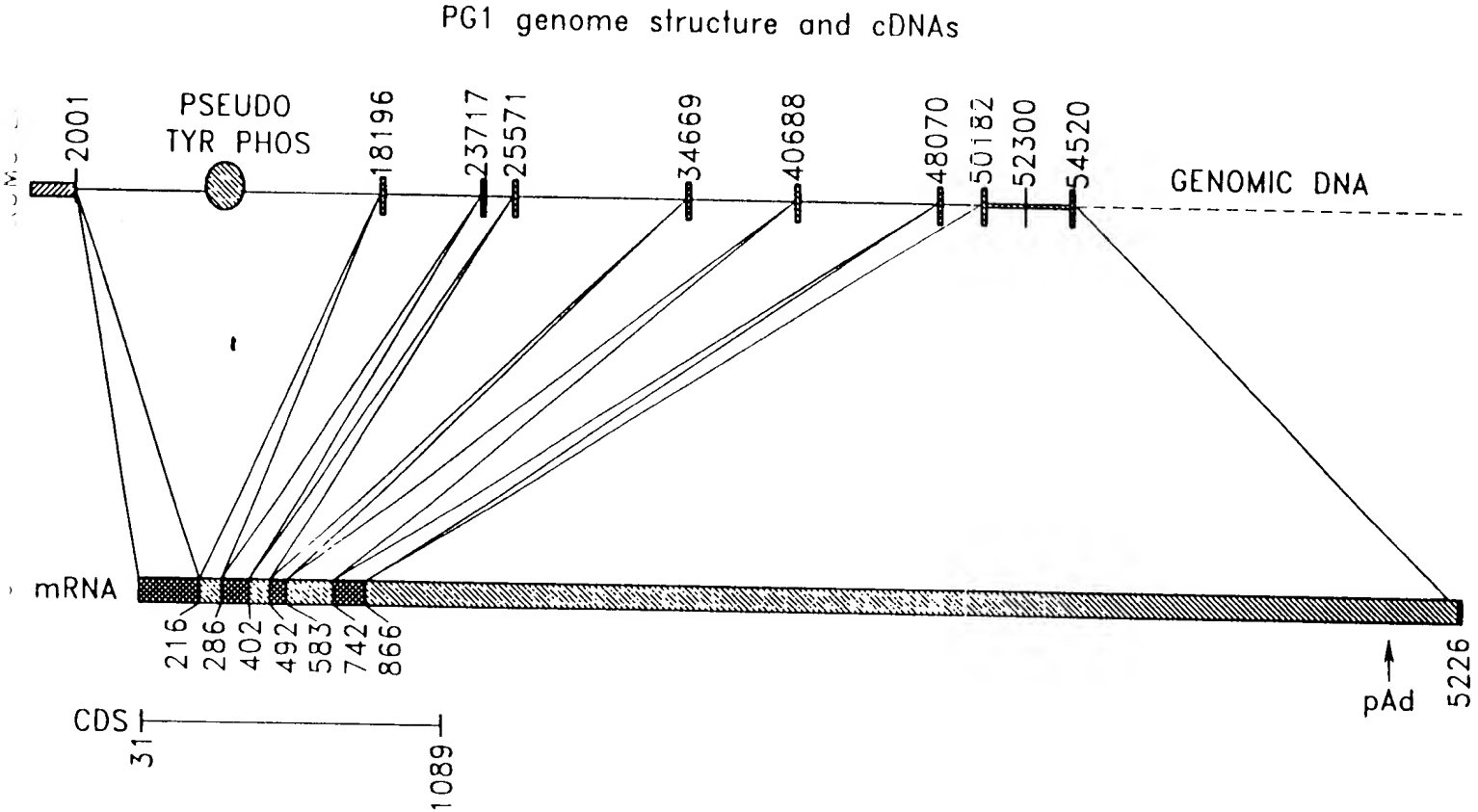
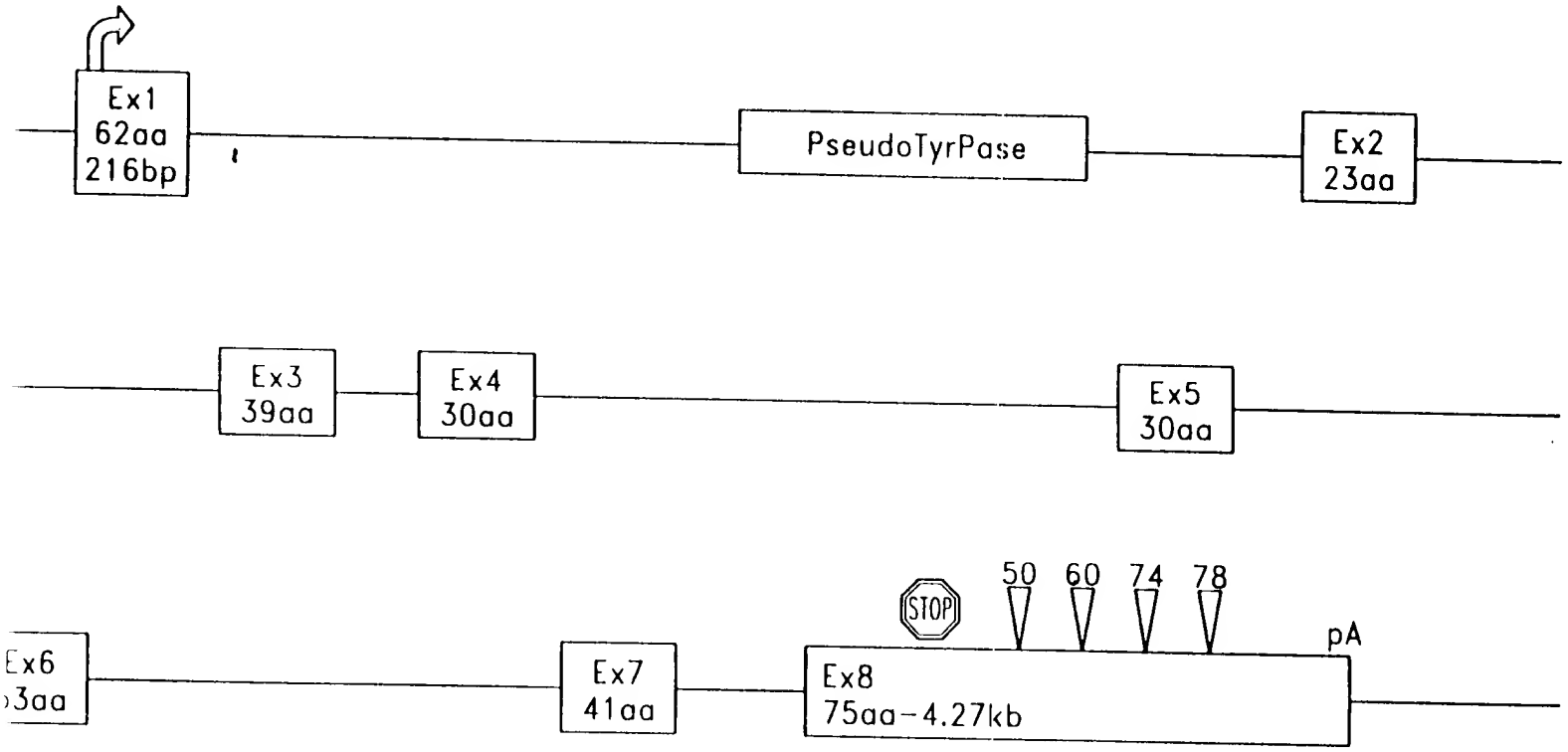

PG1 genome structure and cDNAs
2001
PSEUDO
TYR PHOS
18196
23717
25571
34669
40688
48070
50182
52300
54520
GENOMIC DNA
mRNA
216
286
402
492
583
742
866
pAd
5226
CDS
31
1089

FIG.8

FIG. 8B

Prostate Gene 1



		box 1	box 2	box 3
PG1	Hs	NHQ *81-83*	FPEGTR *160-165*	LDAIYDVTV *211-219*
AF003136 (Genbank)	Ce	NHQ *630-632*	FPEGTR *712-717*	LDAIYDVTV *762-770*
Z72511 (Genbank)	Ce	48 NHR 50	FPEGTD *129-134*	VEYIYDITI *204-212*
P38226 (Swissport)	Sc	111 NHQ 113	FPEGTN *223-228*	IESLYDITI *271-279*
P33333 (Swissport)	Sc	81 NHQ 83	FPEGTR *154-159*	-
Z49770 (Genbank)	Sc	116 NHQ 118	FPEGTN *215-220*	LDAIYDVTI *265-273*
P26647 (Swissport)	Ec	72 NHQ 74	FPEGTR *145-150*	-
Z49860 (Genbank)	Bn	-	FVEGTR *90-95*	VPAIYDMTV *138-146*
U89336 (Genbank)	Hs	95 NHQ 97	FPEGTR *168-173*	-
U56417 (Genbank)	Hs	103 NHQ 105	FPEGTR *176-181*	-
AB005623 (Genbank)	Mm	100 NHQ 102	FPEGTR *173-178*	
Z29518 (Genbank)	Zm	91 NHR 93	FVEGTR *170-175*	VPAIYDTTV *218-226*

Hs = Homo sapiens, Ce = Caenorabibitis elegans, Ec = Escherichia coli;
Sc = Saccharomyces cerevisiae, Bn = Brassica napus, Zm = Zea maize,
Mm = Mus Musculus

- = pattern absent from protein sequence

Note: Funcitional acyl glycerol transferases all contain boxes 1 and 2 and not box 3. Proteins most related to PG1 contain the 3 boxes with a high degree of conservation.

FIG. 9

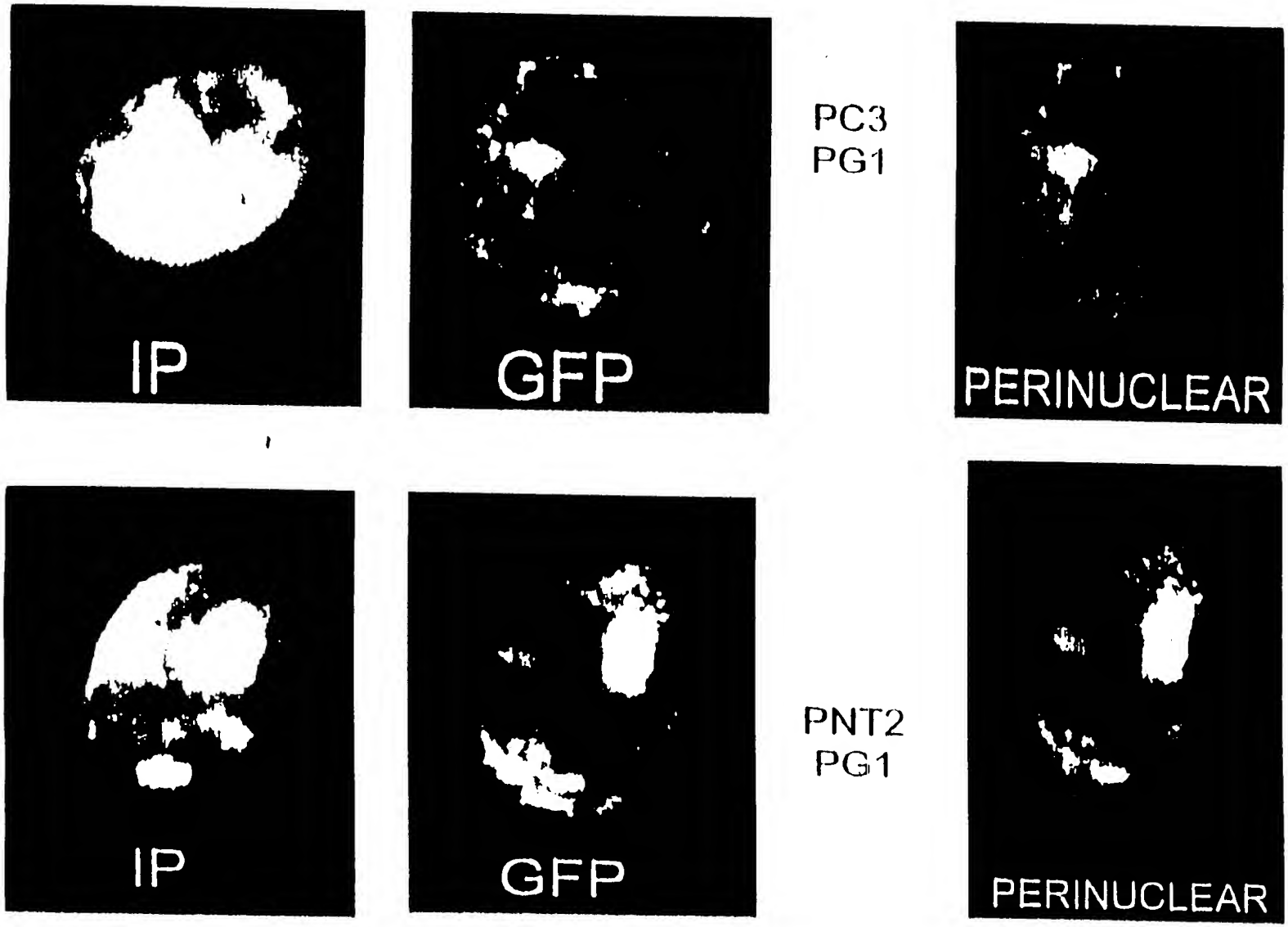


FIG. 10

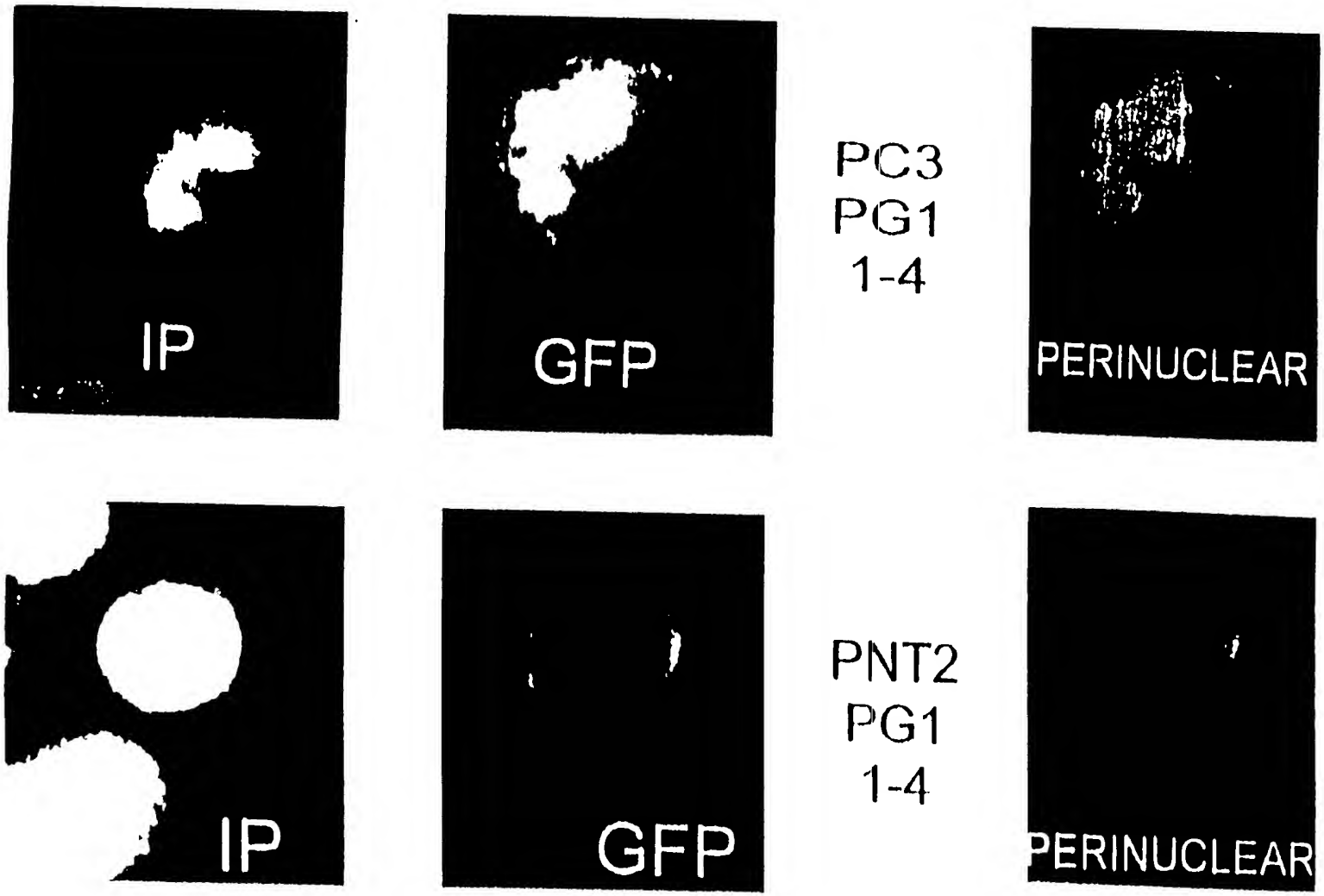


FIG. 11

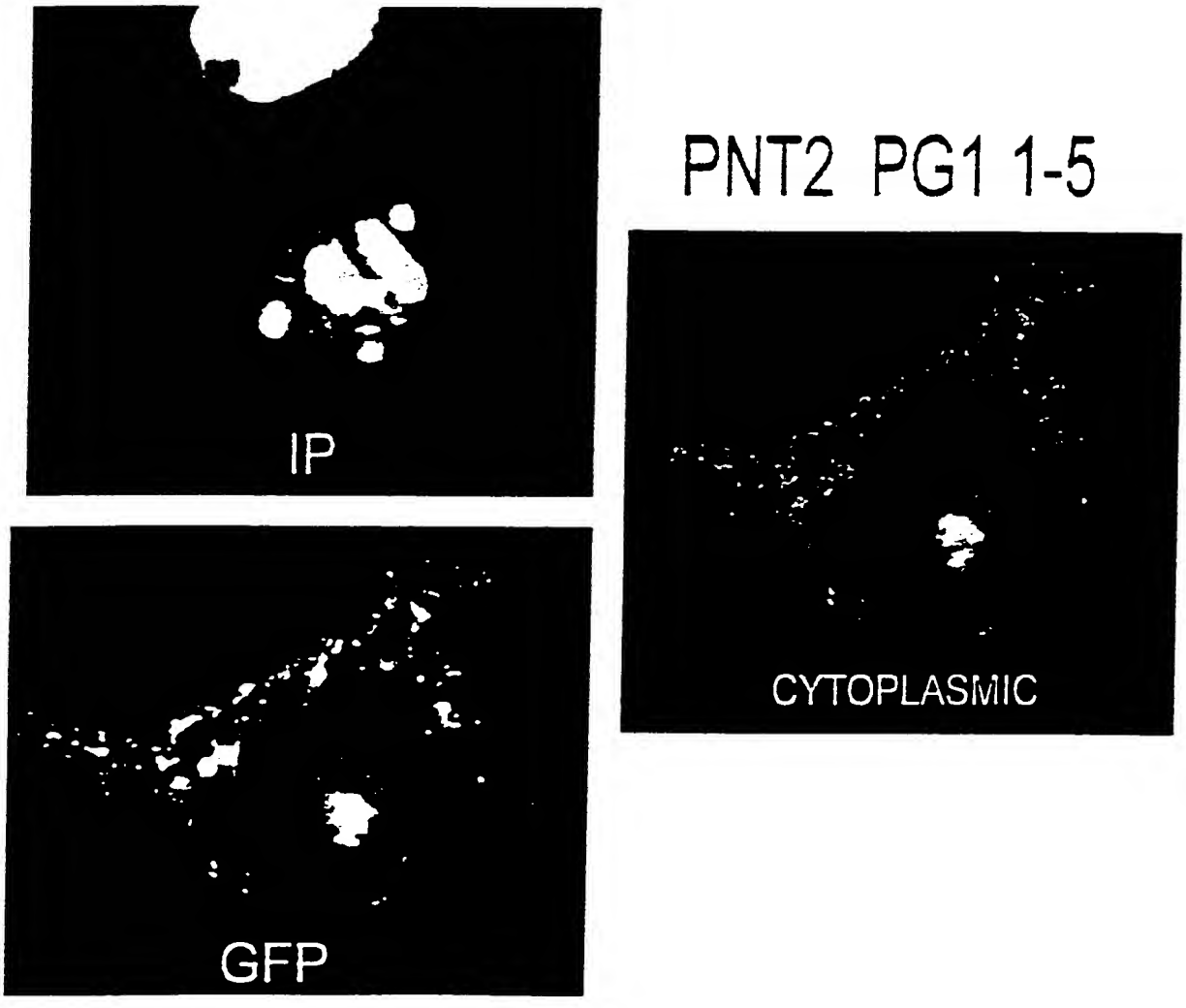
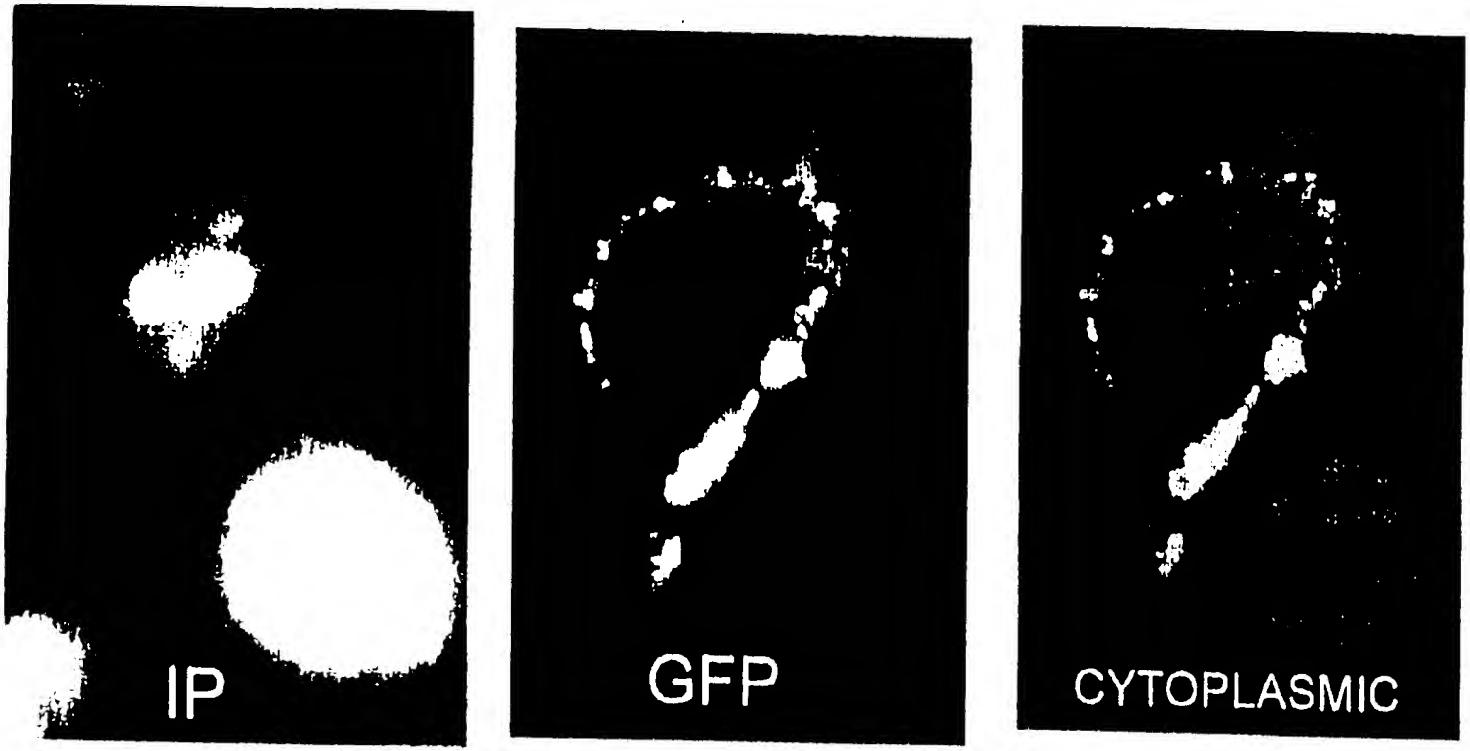


FIG. 2



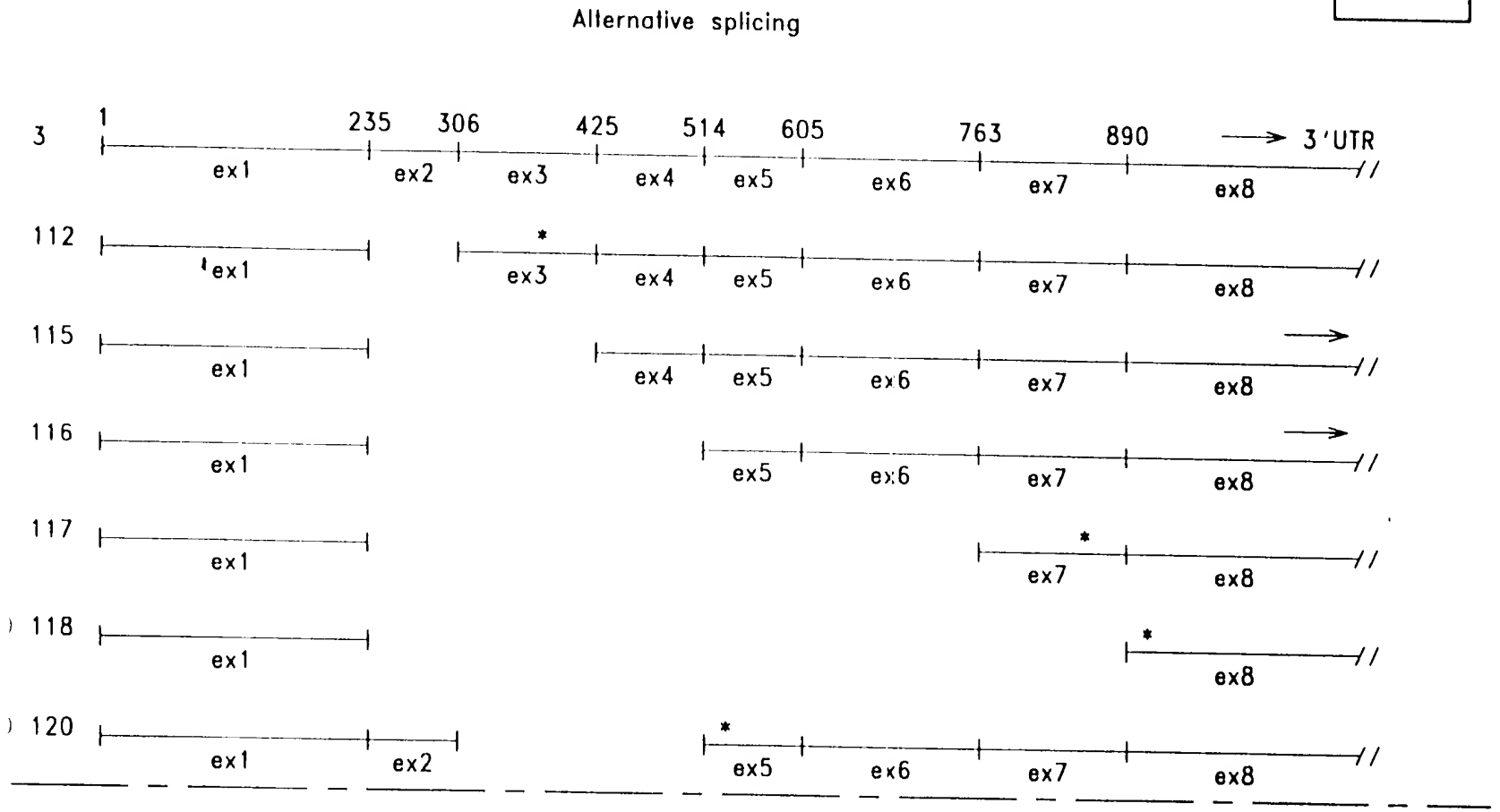
PNT2 PG1 mut229

FIG. 13

FIG. 14A

FIG. 14

FIG. 14A
FIG. 14B



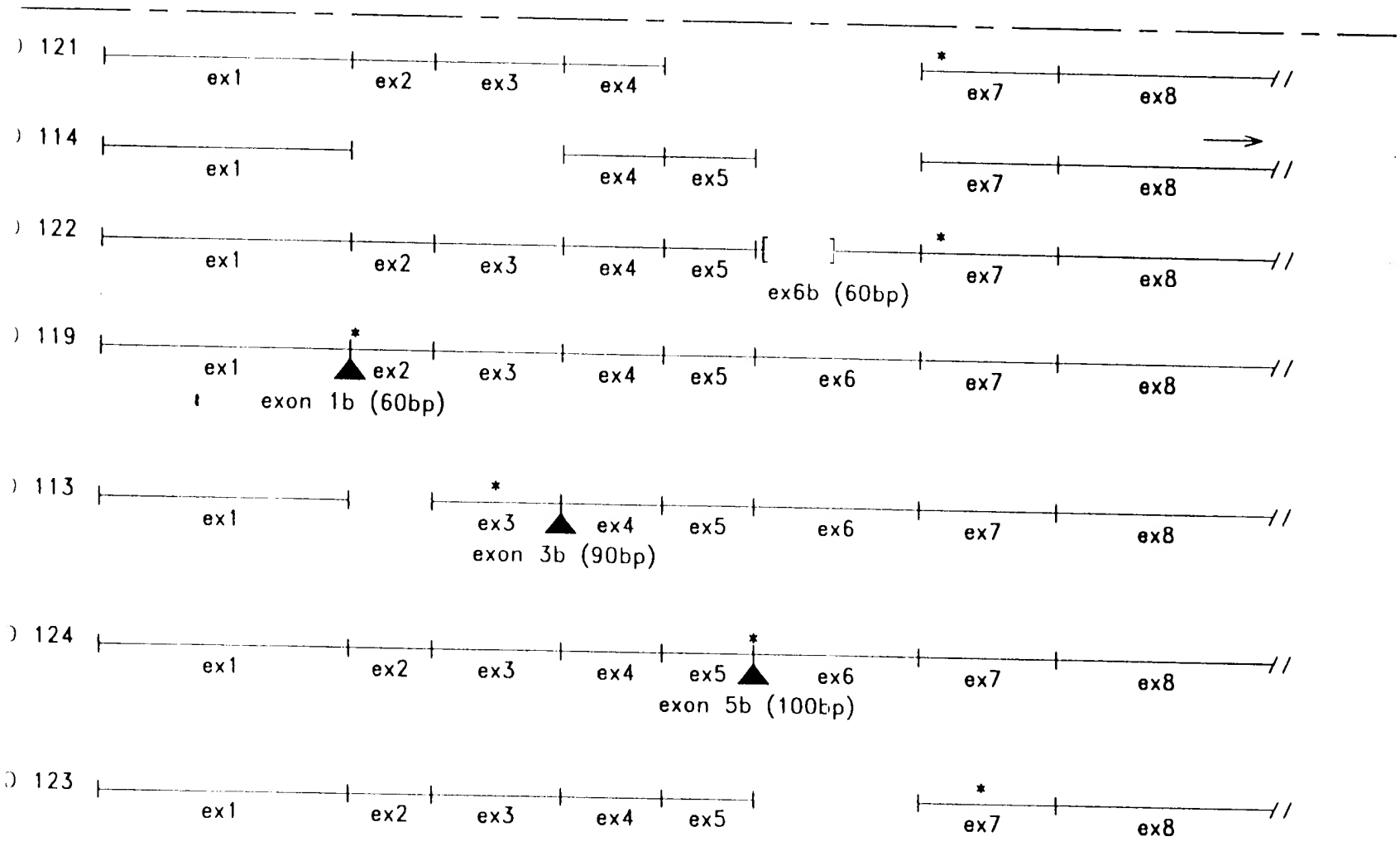

121
ex1
ex2
ex3
ex4
ex7
ex8
114
ex1
ex4
ex5
ex7
ex8
122
ex1
ex2
ex3
ex4
ex5
ex6b (60bp)
ex7
ex8
119
ex1
ex2
exon 1b (60bp)
ex3
ex4
ex5
ex6
ex7
ex8
113
ex1
ex3
exon 3b (90bp)
ex4
ex5
ex6
ex7
ex8
124
ex1
ex2
ex3
ex4
ex5
exon 5b (100bp)
ex6
ex7
ex8
123
ex1
ex2
ex3
ex4
ex5
ex7
ex8

FIG. 14B

Combination of exons of PG1 gene discovered by PCR with primers specific for exon borders

Printer	Clones	prostate	PNT1A	PNT1B	PNT2	LnCaPFCG	LNCaPJMB	CoHPV	Du145	PC3	ECP5	ECP6	ECP7	ECP8	ECP9	ECP10	ECP11	ECP12	ECP13	ECP14	ECP15	ECP16	ECP17	ECP18	ECP19	ECP20	ECP21	ECP22	ECP23	ECP24
PG1exon13	[+]	+	+	+	+	+	[+]	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
PG1exon14	[+]	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
PG1exon15	+	−	−	−	−	−	−	NT	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−
PG1exon16	−	+	−	+	−	−	−	NT	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	+	−	−	−	−
PG1exon17	+	+	+	+	+	+	+	NT	+	+	−	−	+	−	−	−	+	+	+	+	+	+	−	−	+	+	−	−	+	+	−
PG1exon18	+	−	+	+	+	−	−	NT	+	+	−	−	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−
PG1exon24	−	[+]	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
PG1exon25	+	+	−	+	+	−	−	NT	−	−	−	−	−	−	−	+	−	−	−	+	−	−	−	−	−	−	−	−	+	+	−
PG1exon26	−	[+]	−	+	+	+	+	NT	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
PG1exon27	−	−	−	−	−	−	−	NT	+	−	−	−	−	−	−	−	+	−	−	+	−	−	−	−	−	−	−	−	+	+	−
PG1exon28	−	−	+	−	−	−	−	NT	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−
PG1exon35	−	+	+	+	−	+	+	NT	+	+	−	−	−	−	−	+	+	−	+	+	+	−	−	+	+	−	+	−	−	−	−
PG1exon36	−	[+]	+	+	+	+	+	NT	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
PG1exon37	−	−	−	−	−	−	−	NT	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−
PG1exon38	−	−	−	−	−	−	−	NT	−	+	−	−	−	−	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−
PG1exon46	−	[+]	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
PG1exon47	[+]	+	+	+	+	+	+	+	NT	+	+	+	+	+	+	+	−	+	+	−	+	+	+	+	+	+	+	+	+	+	+
PG1exon48	−	−	−	−	−	−	−	NT	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−
PG1exon57	[+]	+	+	+	+	+	+	+	NT	+	+	+	+	+	−	+	−	+	+	+	+	+	+	+	+	+	+	+	+	+	+
PG1exon58	−	−	−	−	−	+	+	NT	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	+	−	−	−	−
PG1exon68	−	−	+	−	−	+	+	NT	+	+	−	−	−	−	+	−	−	−	+	+	−	−	+	−	−	−	+	−	+	+	−
PG1exon1b	+	−	+	+	−	−	−	NT	−	−	−	+	−	−	−	−	+	+	+	−	−	+	−	−	+	−	+	−	−	+	−
PG1exon1b2	+	−	+	+	−	−	−	NT	−	+	−	+	−	−	−	+	+	+	+	−	−	+	−	−	+	−	+	+	−	−	+
PG1exon1b3	[+]	+	−	+	+	+	+	NT	+	+	+	+	−	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
PG1exon1b4	+	−	−	+	−	+	−	−	+	−	−	−	−	+	−	−	−	−	+	−	+	+	−	+	+	−	−	+	−	−	−
PG1exon1b5	+	−	−	+	−	−	−	NT	−	−	−	−	+	−	−	−	−	+	−	−	−	−	+	−	−	−	+	+	−	−	−
PG1exon1b6	[+]	+	−	+	+	+	+	NT	+	+	+	+	+	−	+	−	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
PG1exon1b7	+	−	−	−	−	+	+	NT	−	+	+	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−
PG1exon1b8	−	−	−	+	−	+	−	NT	−	−	−	+	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−
PG1exon3b4	[+]	+	+	−	+	+	+	NT	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
PG1exon3b5	−	−	−	+	−	−	−	NT	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−
PG1exon3b6	[+]	+	+	+	+	+	+	NT	+	+	+	−	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
PG1exon3b7	+	−	+	+	−	−	+	NT	−	+	−	+	−	−	−	−	−	−	−	−	+	+	−	−	+	−	−	−	−	−	−
PG1exon3b8	−	−	−	−	−	−	−	NT	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−
PG1exon5b6	+	+	−	−	−	−	+	NT	−	+	−	+	−	−	−	−	+	+	−	−	−	−	−	−	−	−	−	−	−	−	−
PG1exon5b7	+	−	−	+	+	−	+	NT	+	−	−	−	−	−	−	−	−	−	−	−	+	−	−	−	−	−	−	−	−	−	−
PG1exon5b8	−	−	−	−	−	−	−	NT	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−	−
PG1exon56b	[+]	+	−	+	+	+	+	NT	+	+	+	−	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
PG1exon46b	[+]	+	−	+	+	+	+	NT	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
PG1exon36b	[+]	+	+	+	+	+	+	NT	+	+	+	+	+	−	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
PG1exon26b	[+]	+	+	+	+	+	+	NT	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
PG1exon16b	[+]	+	+	+	+	+	+	NT	+	+	+	+	+	−	+	−	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+

[+] alternative splicing form with combination of exons 13478 instead of 1345678

FIG. 5

FIG. 16

ASSOCIATION STUDIES
HAPLOTYPE FREQUENCY ANALYSIS (chrom 8p23)

POPULATIONS	AFFECTED N= [275;491]	UNAFFECTED N=[130;313]
	ALL CASES	CONTROLS
characteristics of populations	[275,491] all cases	<28 unaffected (65 years or older) & <289 controls (65 years or older with PSA<4)

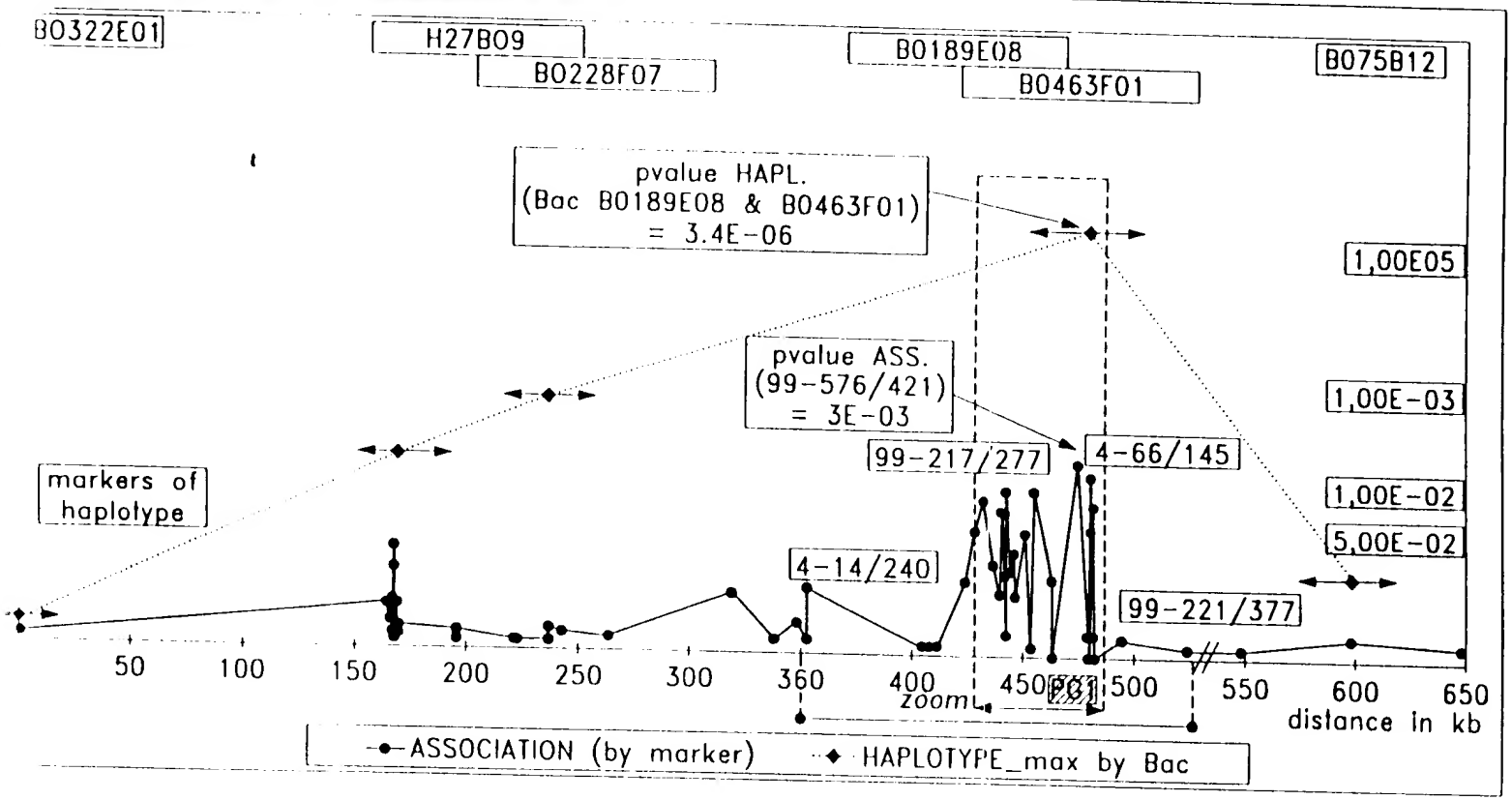
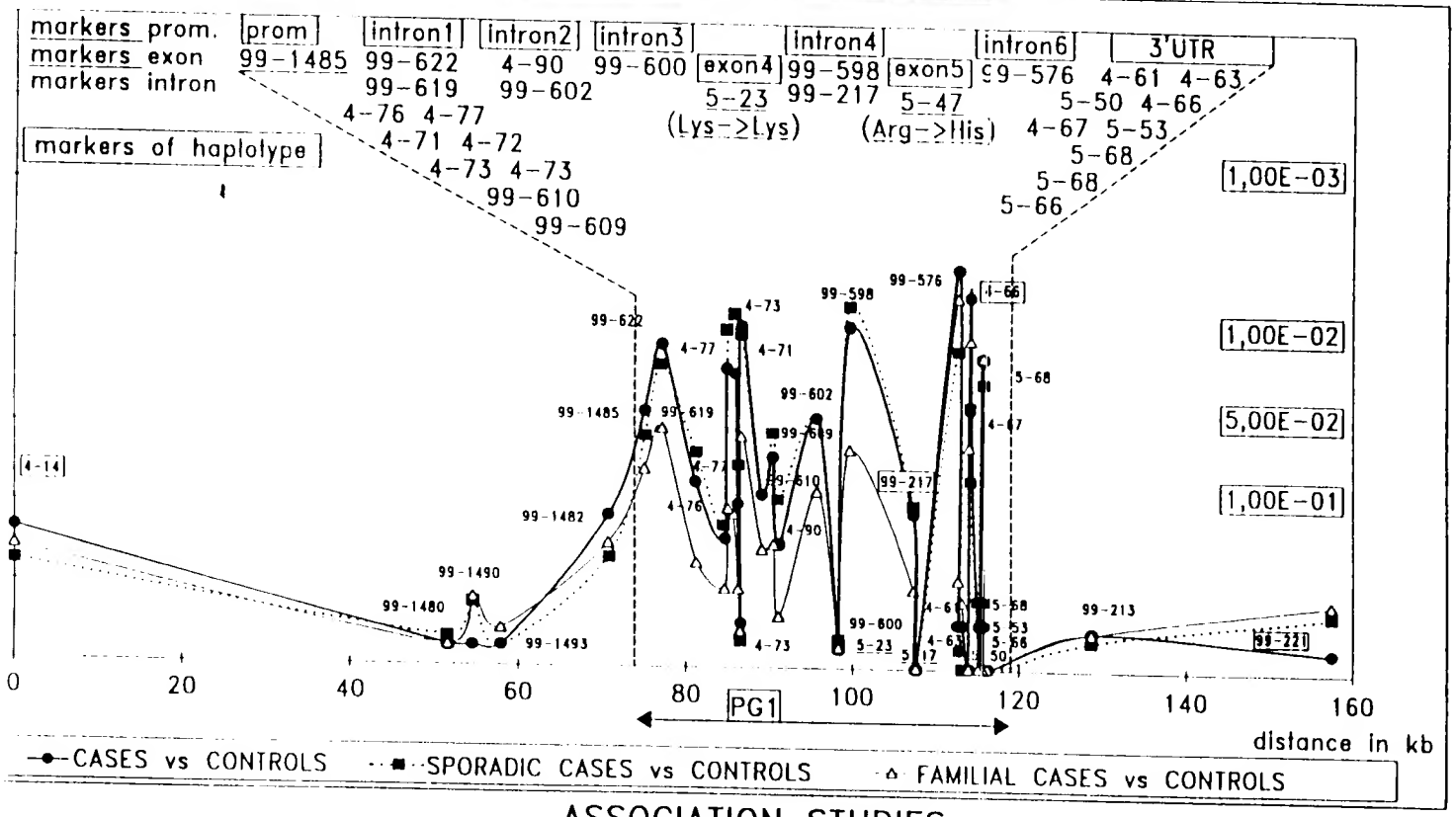


FIG 17

ASSOCIATION STUDIES
PG1 (8p23)

ATIONS	AFFECTED N= [275;491]			UNAFFECTED N=[130;313]
	ALL CASES	SPORADIC CASES	FAMILIAL CASES	CONTROLS
teristics ulations	<=491 all cases	<=294 sporadics cases	<=197 familial cases	<28 unaffected (65 years or older) & <=289 controls (65 years or older with PSA<4)



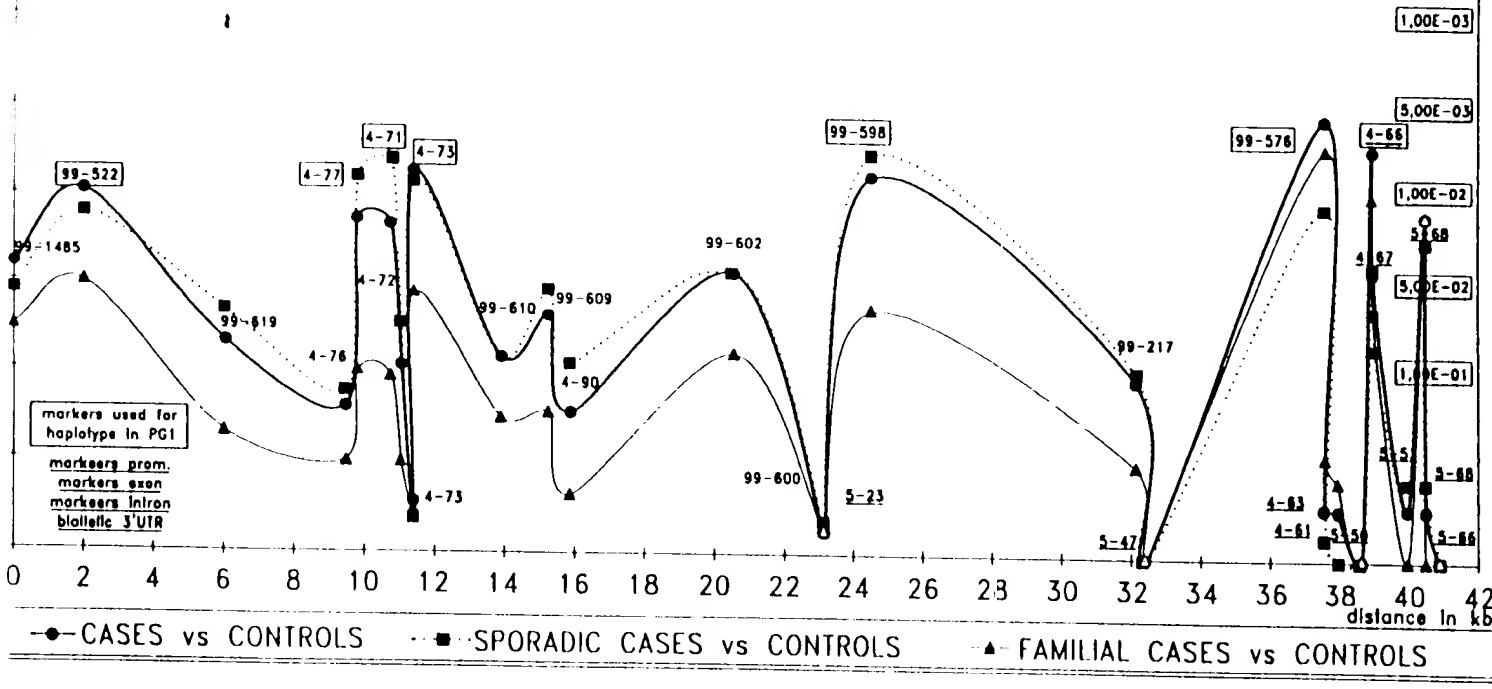
ASSOCIATION STUDIES

FIG. 18A

PG1 (8p23)

ATIONS	AFFECTED N= [275;491]			UNAFFECTED N=[130;313]
	ALL CASES	SPORADIC CASES	FAMILIAL CASES	CONTROLS
teristics ulations	<=491 all cases	<=294 sporadics cases	<=197 familial cases	<28 unaffected (65 years or older) & <=289 controls (65 years or older with PSA<4)

prom	intron1	intron2	intron3	exon4	intron4	exon5	intron6	3'UTR
99-1485	99-622 99-619 4-76 4-77 4-71 4-72 4-73 4-73 99-610 99-609	4-90 99-602	99-600	5-23 (Lys->Lys)	99-598 99-217	5-47 (Arg->His)	99-576	4-61 4-63 5-50 4-66 4-67 5-53 5-68 5-68 5-66



e of kers	PG1	Polym.	Freq(cas)	Freq(controls)	abs diff % (fq(cases)-(fq(controls))	Odd Ratio	Pvalue	Freq(randoms)	Attributable Risk
5/251	prom	G*/T	0.32	0.24	7.4	1.44	2.53E-02	0.29	17.58
/95	in1	G/T	0.52	0.42	10.1	1.51	9.64E-03	ND$	ND
/141	in1	C/T	0.28	0.22	5.8	1.37	6.93E-02	ND	ND
2	in1	G/A	0.43	0.38	5	1.23	1.57E-01	0.41	13.15
1	in1	G/C	0.34	0.26	7.4	1.43	1.35E-02	0.31	18.16
3	in1	A/G	0.34	0.26	8.3	1.49	1.43E-02	0.28	18.64
7	in1	A/G	0.36	0.30	5.7	1.29	9.43E-02	0.31	13.25
4	in1	G/C	0.52	0.42	9.7	1.48	7.29E-03	0.52	26.76
/250	in1	G/A	0.43	0.37	6.2	1.30	8.33E-02	ND	ND
/225	in1	A/T	0.37	0.30	7	1.36	4.83E-02	ND	ND
83	in2	A/C	0.29	0.25	4.4	1.25	1.68E-01	0.28	9.32
/258	in2	A/G	0.33	0.25	7.4	1.44	2.69E-02	ND	ND
/492	in3	T/A	0.34	0.34	0.3	1.01	7.52E-01	ND	ND
/130	in4	G/A	0.35	0.25	9.2	1.55	7.29E-03	ND	ND
/277	in4	T/C	0.31	0.28	3.8	1.20	1.07E-01	0.28	8.46
/421	in6	G/C	0.27	0.17	9.2	1.72	3.18E-03	0.24	18.40
69	3'UTR	G/A	0.01	0.00	0.3	1.76	0,527 §	ND	ND
45	3'UTR	C/T	0.25	0.19	6.2	1.43	4.68E-03	0.24	13.16
	3'UTR	T/C	0.25	0.20	4.9	1.33	2.39E-02	0.24	10.97

§ Test Fisher-$ ND: Not done -* disease associated allele / not associated allele

FIG. 18B

FIG. 19A

HAPLOTYPE FREQUENCY ANALYSIS

POPULATIONS	AFFECTED	UNAFFECTED
sample sizes	CASES (n=491)	CONTROLS (n=317)
characteristics of populations	294 sporadic cases + 197 familial cases	28 unaffected (65 years or older) + 289 controls (65 years or older with PSA<4)

PG1 (8p23)			4-14/240	99-217/277	4-66/145	99-221/377
				in4	3'UTR	
distance between mks				<100kb>	<17kb>	<43kb>
size (cases vs controls)			481vs305	481vs302	481vs300	481vs303
frequency % (cases/controls)			65,7/62,1(C)	31,3/27,5(C)	25,1/19(C)	42,7/42,91 (A)
abs diff freq. all.(cases-controls)			3.6	3.8	6.2	0
pvalue			1.47E-01	1.07E-01	4.68E-03	7.52E-01
Hardy Weinberg Disequilibrium		cases	5.84E-01	6.55E-01	2.54E-01	5.84E-01
		controls	4.80E-01	2.21E-01	3.71E-01	2.54E-01
HAP 1 <43kb>		451 vs 297			C	A
HAP 2 <17kb>		451 vs 296		T	C	
HAP 3 <117kb>		452 vs 299	C		C	
HAP 4 <100kb>		479 vs 302	C	T		
HAP 5 <60kb>		476 vs 300		T		A
HAP 6 <160kb>	PT2	476 vs 303	C			C
HAP 7 <160kb>		447 vs 297	C		C	A
HAP 8 <60kb>		446 vs 294		T	C	A
HAP 9 <117kb>		450 vs 296	C	T	C	
HAP 10 <160kb>	PT3	474 vs 300	C	T		A
HAP 11 <160kb>	PT4	445 vs 294	C	T	C	A

haplotype frequencies		Odd ratio	Chi-S	Pvalue	
cases	controls				
0.116	0.067	1.83	9.85	(1.7e-03)	***
0.243	0.183	1.43	7.49	(6.2e-03)	**
0.182	0.130	1.49	7.18	(7.3e-03)	**
0.217	0.188	1.20	1.88	(1.7e-01)	*
0.155	0.132	1.20	1.54	(2.1e-01)	*
0.373	0.346	1.12	1.16	(2.7e-01)	*
0.095	0.042	2.39	14.62	(1.3e-04)	****
0.117	0.065	1.93	11.33	(7.3e-04)	***
0.095	0.032	3.18	21.59	(3.4e-06)	*****

FIG. 19B

HAPLOTYPE FREQUENCY ANALYSIS

PG1 (8p23)

markers of haplotype Max	4-14/240	99-217/277 in4	4-66/145 3'UTR	99-221/377
	C	T	C	A
distance between mks	<100kb>	<17kb>	<43kb>	

PG1	sample sizes	haplotype frequencies		odd ratio	chi-S	P value	
	cases vs control	cases	controls				
s control	455 vs 294	0.095	0.032	3.18	21.59	3.40E-06	******
(<=65 years) vs controls	171 vs 294	0.105	0.032	3.56	20.91	4.60E-06	******
(>65 years) vs control	271 vs 294	0.079	0.032	2.60	12.13	4.80E-04	****
c cases vs controls	266 vs 294	0.096	0.032	3.23	19.73	8.60E-06	******
dic cases (<=65 years) vs controls	85 vs 294	0.095	0.032	3.20	12.04	5.00E-04	****
dic cases (>65 years) vs controls	178 vs 294	0.085	0.032	2.82	12.75	3.50E-04	****
mative sporadic cases vs controls	67 vs 294	0.062	0.032	2.00	2.70	9.40E-02	**
cases vs controls	179 vs 294	0.098	0.032	3.32	18.33	1.80E-05	*****
al cases (<=65 years) vs controls	86 vs 294	0.112	0.032	3.83	17.98	2.20E-05	*****
al cases (>65 years) vs controls	93 vs 294	0.075	0.032	2.48	6.59	1.00E-02	**
ial cases (>=3 caP) vs controls	79 vs 294	0.123	0.032	4.26	21.33	3.70E-06	******

FIG. 20

HAPLOTYPE FREQUENCY ANALYSIS (PG1)

Markers in PG1			99-622/95	4-77/151	4-71/233	4-73/134	99-598/130	99-576/421	4-66/145	haplotype frequencies		Odd Ratio	Attributable Risk %	Pvalue (cases vs controls)	
			G/T	C/G	A/G	C/G	A/G	C/G	C/T						
			In1				In4	In6	3'UTR						
size (cases vs controls)			336 vs 108	363 vs 173	336 vs 130	352 vs 129	347 vs 126	355 vs 129	456 vs 306						
c frequency % (cases / controls)			52/42 (G)	34/26 (G)	34/26 (A)	52/42 (G)	35/25 (G)	27/17 (G)	25/19 (C)						
allelic frequency % (randoms)			ND	31 (G)	28 (A)	52 (G)	ND	24 (G)	24 (C)						
f freq all. % (cases-controls)			10 1	7 4	8 3	9 7	9 2	9.2	6 2						
pvalue (cases vs controls)			9.64E 03	1 35E-02	1 43E-02	7 29E 03	7 29E 03	3 18E-03	4 68E 03						
			..	..	..	..	..	...	...						
Odd Ratio			1 51	1 43	1 49	1 48	1 55	1 72	1 43						
Attributable Risk %			ND	18 16	18 64	26 76	ND	8 46	13 16						
ardy feberg uilibrium	cases		7 52E-01	7.52E-01	5 84E-01	7 52E-01	7.52E-01	7 52E-01	3 43E-01						
	controls		4 39E 01	4 03E-01	1 21E-01	7 52E 01	6 52E-02	7 52E 01	1 29E-01						
type 1	2 MKS	339 vs 167	G						G	0.263	0.152	1.99	18.55	(6.7e-05)	****
type 2	3 MKS	330 vs 122					G	G	G	0 259	0 147	2 02	ND	(3 9e 04)	***
type 3	4 MKS	312 vs 122			A		G	G	G	0 259	0 147	2 02	ND	(4 1e 04)	***
type 4	5 MKS	311 vs 121			A	G	G	G	G	0 26	0 148	2 01	ND	(4 8e 04)	***
type 5	6 MKS	309 vs 121		G	A	G	G	G	G	0 258	0 149	2	ND	(5 3e 04)	***
type 6	7 MKS	290 vs 99	G	G	A	G	G	G	G	0 255	0 146	2	ND	(1 6e 03)	***

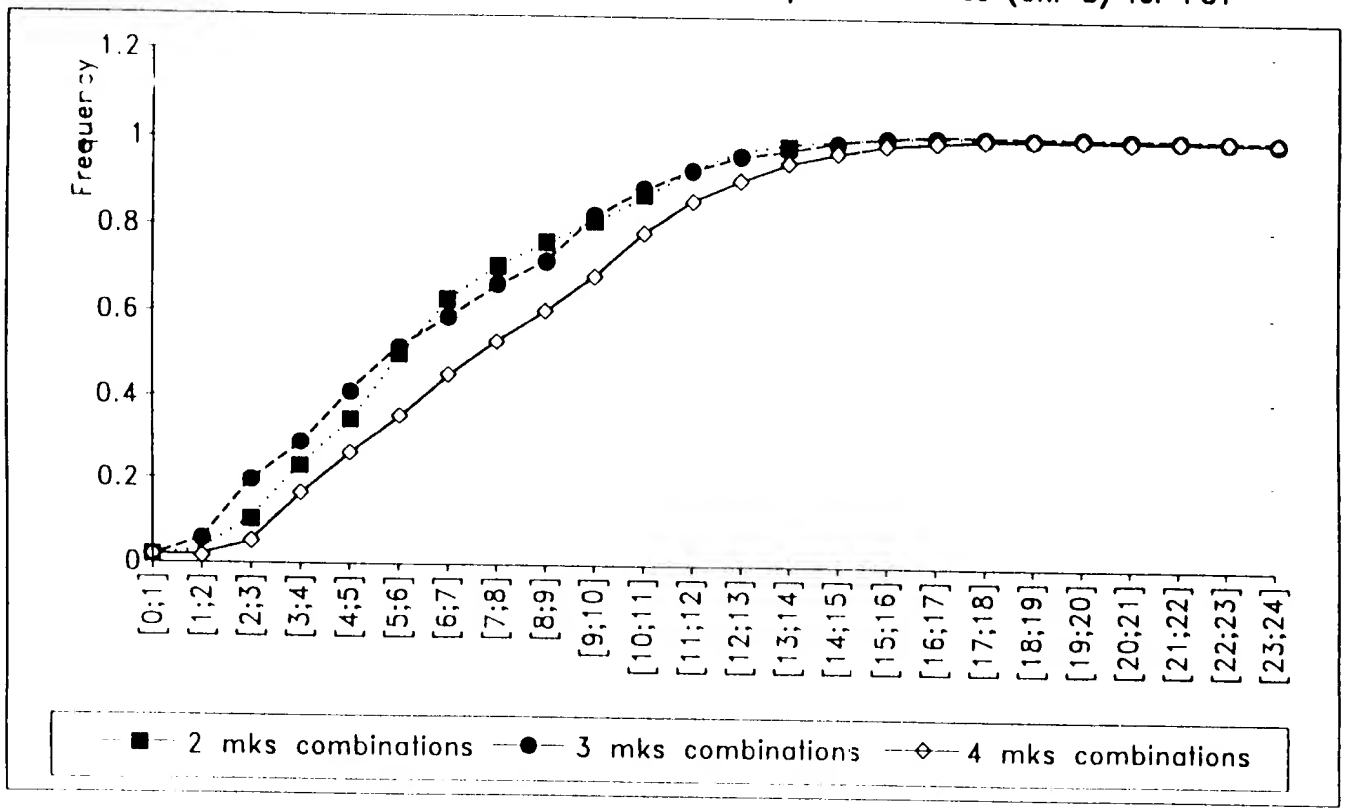
ND Not Done

FIG. 21

Comparison of Pvalue between nb of mks for haplotype (19 mks of PG1)

GENE	# of markers	# of 2 mks combinations	# of 3 mks combinations	# of mks combinations
PG1	19	171	969	3876

CUMULATIVE FREQUENCY HISTOGRAM OF Chi-square statistics (Chi-S) for PG1



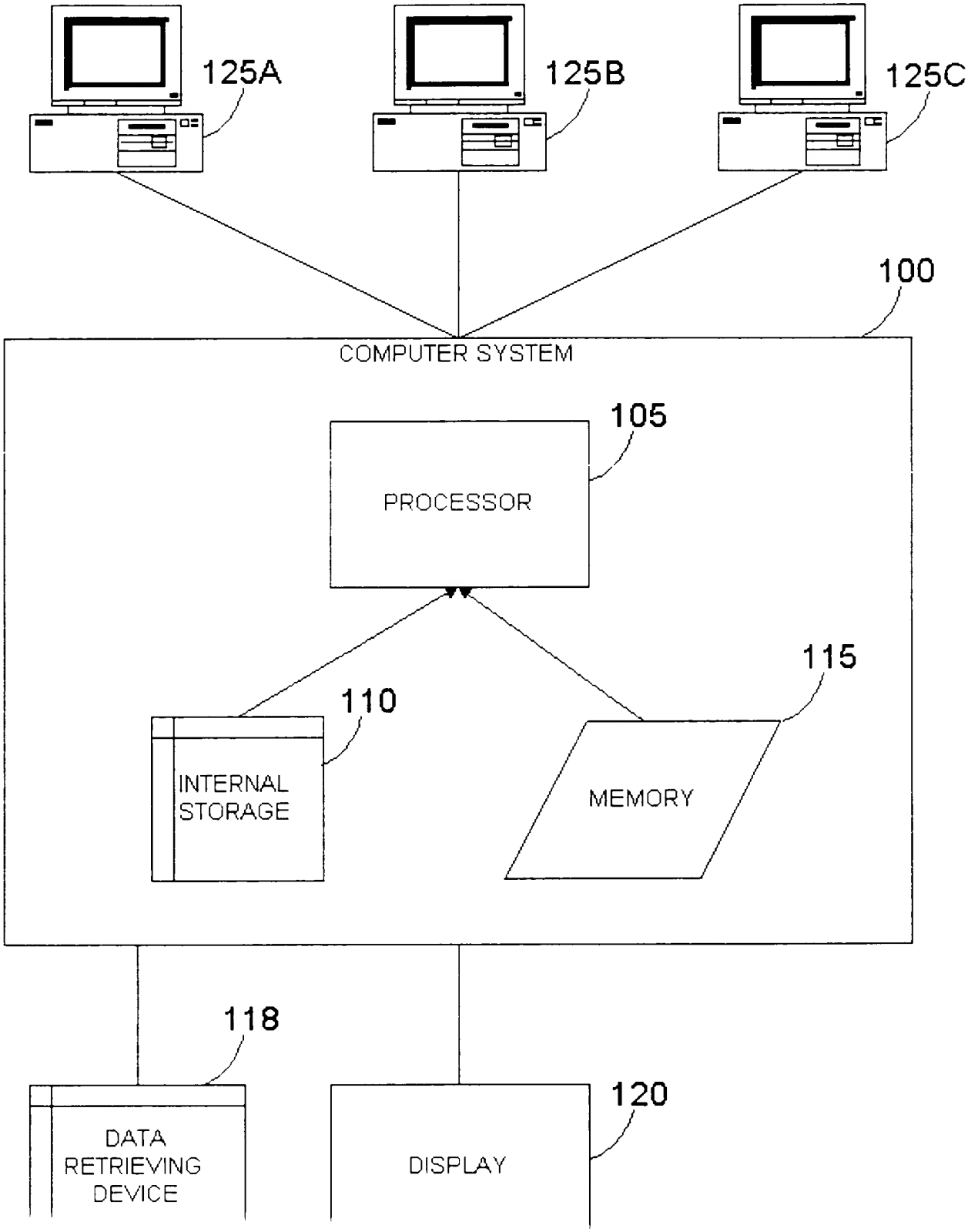

125A
125B
125C
100
COMPUTER SYSTEM
105
PROCESSOR
115
110
INTERNAL STORAGE
MEMORY
118
DATA RETRIEVING DEVICE
120
DISPLAY

FIG. 22

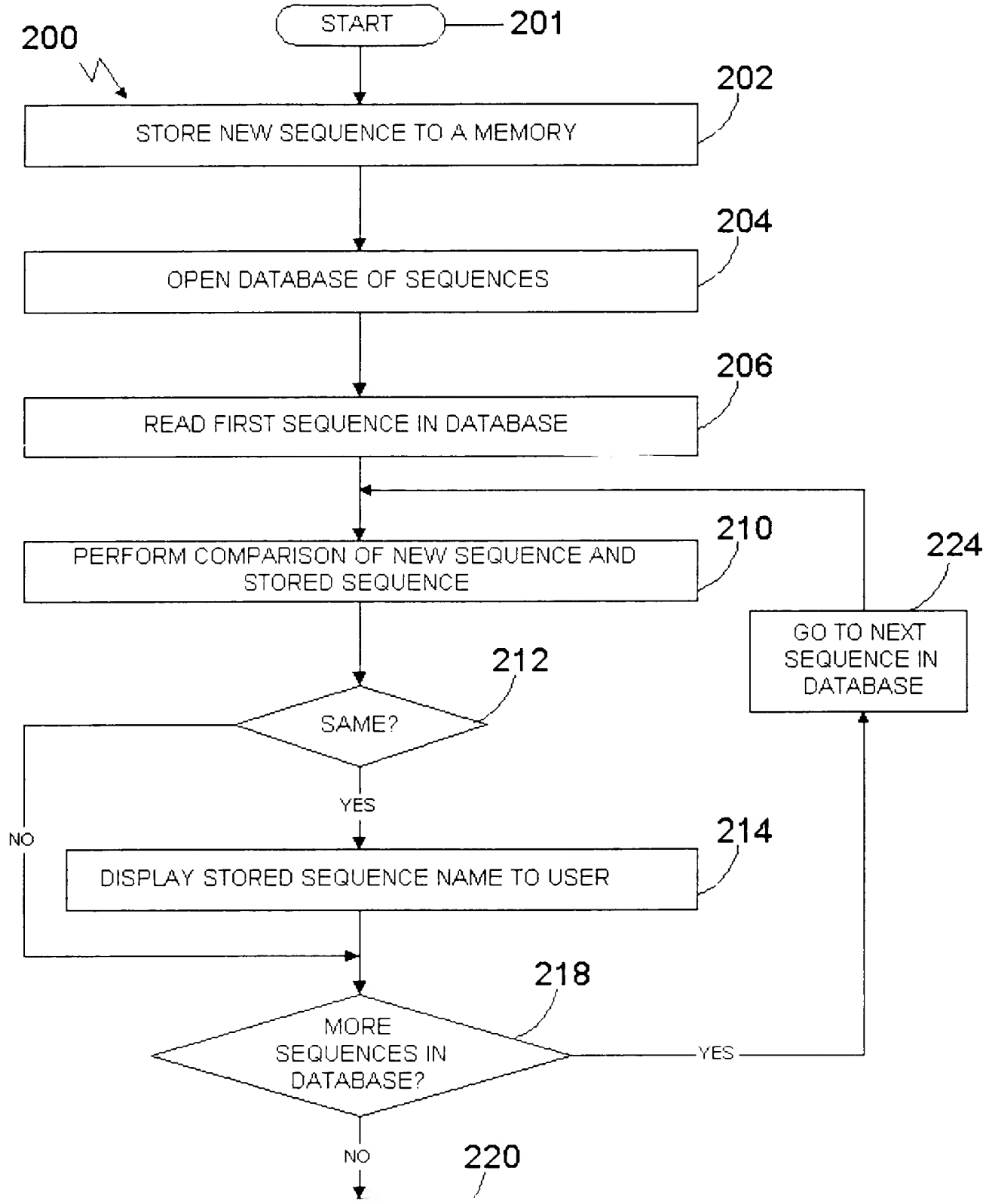

START
201
200
202
STORE NEW SEQUENCE TO A MEMORY
204
OPEN DATABASE OF SEQUENCES
206
READ FIRST SEQUENCE IN DATABASE
210
PERFORM COMPARISON OF NEW SEQUENCE AND STORED SEQUENCE
224
GO TO NEXT SEQUENCE IN DATABASE
212
SAME?
YES
NO
214
DISPLAY STORED SEQUENCE NAME TO USER
218
MORE SEQUENCES IN DATABASE?
YES
NO
220

FIG. 2C

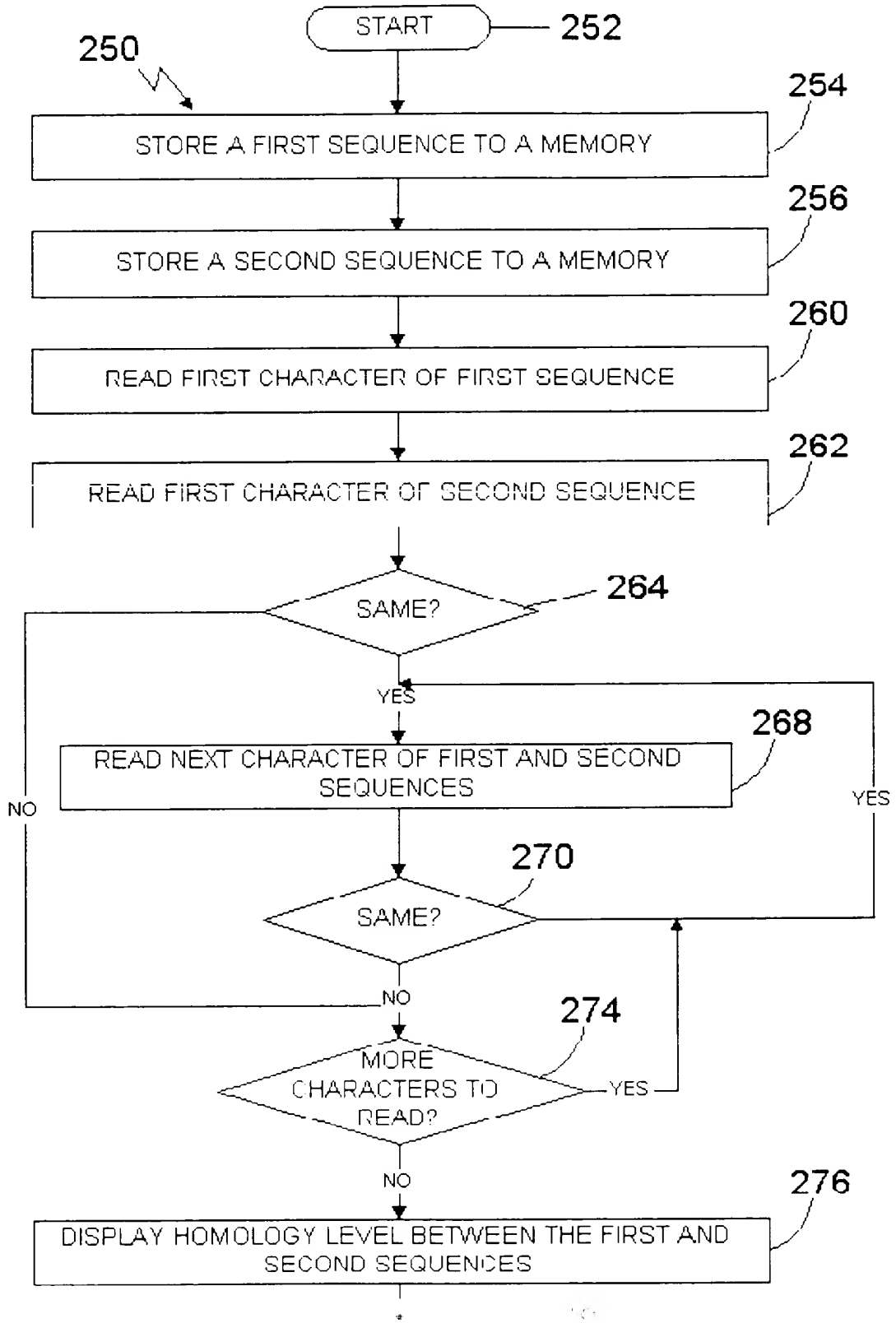

START
252
250
254
STORE A FIRST SEQUENCE TO A MEMORY
256
STORE A SECOND SEQUENCE TO A MEMORY
260
READ FIRST CHARACTER OF FIRST SEQUENCE
262
READ FIRST CHARACTER OF SECOND SEQUENCE
264
SAME?
YES
NO
268
READ NEXT CHARACTER OF FIRST AND SECOND SEQUENCES
YES
270
SAME?
NO
274
MORE CHARACTERS TO READ?
YES
NO
276
DISPLAY HOMOLOGY LEVEL BETWEEN THE FIRST AND SECOND SEQUENCES

FIG. 24

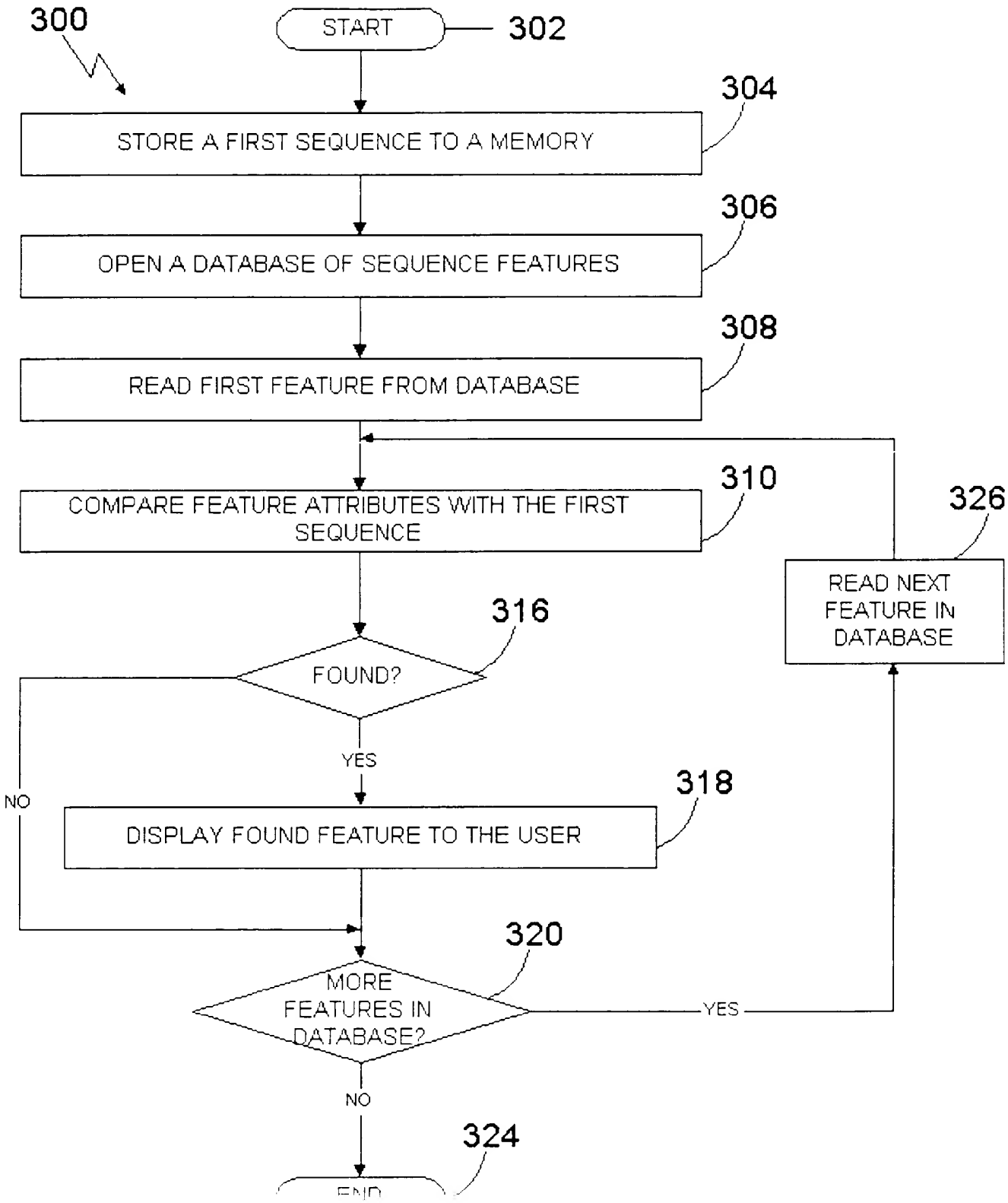

300
START
302
304
STORE A FIRST SEQUENCE TO A MEMORY
306
OPEN A DATABASE OF SEQUENCE FEATURES
308
READ FIRST FEATURE FROM DATABASE
310
COMPARE FEATURE ATTRIBUTES WITH THE FIRST SEQUENCE
326
READ NEXT FEATURE IN DATABASE
316
FOUND?
YES
NO
318
DISPLAY FOUND FEATURE TO THE USER
320
MORE FEATURES IN DATABASE?
YES
NO
324
END

FIG 3